



Search Report

EIC 1600

STIC Database Tracking Number: 235315

To: LOUIS WOLLENBERGER
Location: REM-2A05 / Mailbox 2C18
Art Unit: 1635
Monday, August 27, 2007

Case Serial Number: 10/709691

From: TOBY PORT
Location: EIC 1600
REM-1D58 / REM-1A59
Phone: (571)272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner WOLLENBERGER:

Enclosed are the results of an alignment search for the two sequences. The database search for these two sequences is still processing and the results will appear in SCORE after it has completed.

If you have any questions, please don't hesitate to call me.

Thank you for using STIC search services.

Toby Port
x22523

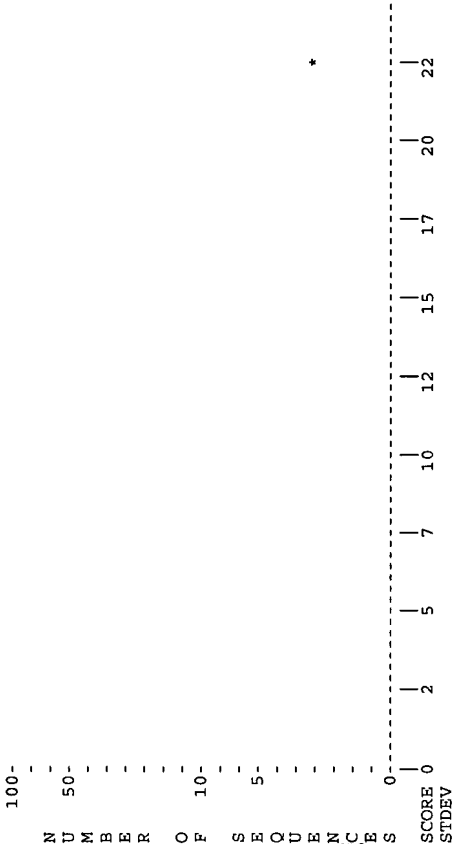


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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq348.res made by tport on Mon 27 Aug 107 14:17:29-PDT.

Query sequence being compared: SEQ348.SEQ (1-22)
Number of sequences searched: 2
Number of scores above cutoff: 2
Results of the initial comparison of SEQ348.SEQ (1-22) with:
File : wol691.seq



PARAMETERS

Similarity matrix Unitary K-tuple 4
Mismatch penalty 1 Joining penalty 30
Gap penalty 5.00 Window size 22
Gap size penalty 0.33
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 22 Median 23 Standard Deviation 0.00
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 113
Number of sequences searched: 2
Number of scores above cutoff: 2

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Length	Score	Sig.	Frame
1. SEQ348.SEQ	Entered [tport 27-Aug-07 14:11]	22	22	22	0.00 0

1. SEQ348.SEQ Entered [tport 27-Aug-07 14:11] 22 22 22 0.00 0
A 100% similar sequence to the query sequence was found:

Sequence Name	Description	Length	Score	Sig.	Frame
2. SEQ4233864.SEQ	Entered [tport 27-Aug-07 14:11]	91	22	22	0.00 0

1. SEQ348.SEQ (1-22)
SEQ348.SEQ Entered [tport 27-Aug-07 14:10]
Initial Score = 22 Optimized Score = 22 Significance = 0.00
Residue Identity = 100% Matches = 22 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

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CAGCAGCACACUGUGGUUGUA
X 10 20 X

2. SEQ348.SEQ (1-22)
SEQ4233864.SEQ Entered [tport 27-Aug-07 14:11]
Initial Score = 22 Optimized Score = 22 Significance = 0.00
Residue Identity = 100% Matches = 22 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X 10 20 X
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CCUGCUCGCCCGCCAGCAGCACACUGUGGUUGUACGGCACUGUGGCCACGCUCCAACACACUGUGGUGU
10 X 20 30 X 40 50 60 70
AGAGCGAGGGUGG
80